

SEQUENCE LISTING

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<120> EUKARYOTIC PEPTIDE UPTAKE SYSTEM FOR TRANSPORTING ENKEPHALINS

<130> 1046-PCT-00

<140> 09/914541

<141> 2001-08-29

<150> PCT/US00/05158

<151> 2000-03-01

<150> 60/122, 312

<151> 1999-03-01

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<170> PatentIn Ver. 2.1

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Ala Thr Thr Asp Glu Glu Asp Arg Asp Pro Glu Ser Gln Lys Phe Asp
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Arg His Ser Ile Gln Glu Glu Gly Leu Val Trp Lys Gly Asp Pro Thr
65 70 75 80

Tyr Leu Pro Asn Ser Pro Tyr Pro Glu Val Arg Ser Ala Val Ser Ile
85 90 95

Glu Asp Asp Pro Thr Ile Arg Leu Asn His Trp Arg Thr Trp Phe Leu
100 105 110

Thr Thr Val Phe Val Val Phe Ala Gly Val Asn Gln Phe Phe Ser
115 120 125

Leu Arg Tyr Pro Ser Leu Glu Ile Asn Phe Leu Val Ala Gln Val Val
130 135 140

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145 150 155 160

Ser Lys Val Pro Phe Phe Asp Leu Asn Pro Gly Pro Phe Thr Lys Lys
165 170 175

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325 330 335

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Val Leu Pro Cys Leu Tyr Phe Thr Asn Thr Trp Tyr Ala Lys Tyr Met
370 375 380

Pro Val Ile Ser Gly Ser Thr Tyr Asp Asn Thr Gln Asn Lys Tyr Asn
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Val Thr Lys Ile Leu Asn Glu Asp Tyr Ser Ile Asn Leu Glu Lys Tyr
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Lys Glu Tyr Ser Pro Val Phe Val Pro Phe Ser Tyr Leu Leu Ser Tyr
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Ala Leu Asn Phe Ala Ala Val Ile Ala Val Phe Val His Cys Ile Leu
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Tyr His Gly Lys Asp Ile Val Ala Lys Phe Lys Asp Arg Lys Asn Gly
450 455 460

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485 490 495

Phe Val Ala Val Cys Cys Phe Asp Thr Lys Phe Pro Ala Trp Ala Phe
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Lys Leu Met Ala Thr Thr Leu Pro Thr Thr Lys Leu Arg Leu Pro Gly
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His Val Leu Ile Thr Ile Phe Ala Asn Thr Gly Ala Gly Gly Ala Tyr
130 135 140

Ala Thr Ser Ile Leu Thr Ile Val Lys Ala Phe Tyr His Arg Asn Leu
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Asn Pro Ala Ala Ala Met Leu Leu Val Gln Thr Thr Gln Leu Leu Gly
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His Glu Lys Glu Glu Lys Arg Glu Gly Lys Gln Thr Lys Leu Arg Phe
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325 330 335

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340 345 350

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385 390 395 400

Glu Leu Trp Lys Lys Ala Thr Leu Thr Thr Lys Asp Lys Phe Gly Asp
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Cys Glu Gly Phe Gly Lys Gln Leu Gln Leu Pro Trp Trp Gly Leu Leu
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Lys Thr Tyr Gly Ser Val Ser Ile Ala Gln Ala Leu Tyr Phe Val Gly
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Asp Phe Lys Leu Gly His Tyr Met Lys Ile Pro Pro Arg Ser Met Phe
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Met Leu Pro Lys Ser Ser Pro Trp Thr Cys Pro Gly Asp Val Val Phe
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Tyr Asn Ala Ser Ile Ile Trp Gly Ile Ile Gly Pro Gly Arg Met Phe
595 600 605

Thr Ser Lys Gly Ile Tyr Pro Gly Met Asn Trp Phe Phe Leu Ile Gly
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Phe Leu Ala Pro Val Pro Val Trp Phe Phe Ala Arg Lys Phe Pro Glu
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Lys Lys Trp Ile His Gln Ile His Ile Pro Leu Ile Phe Ser Gly Ala
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Trp Ala Arg His Asn Tyr Ile Leu Ser Ala Ala Leu Asp Ala Gly Thr
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Ala Val Met Gly Val Leu Ile Tyr Phe Ala Leu Gln Asn Asn Asn Ile
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Pro Ser Gln Pro Ser Leu Met Gln Ile Ala Gly Leu Pro Ile Gly Lys
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Phe Met Ala Arg Thr Leu Pro Thr Thr Ser His Asn Leu Leu Gly Trp
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Ser Phe Ser Leu Asn Pro Gly Pro Phe Asn Ile Lys Glu His Val Ile
85 90 95

Ile Thr Ile Phe Ala Asn Cys Gly Val Ala Tyr Gly Gly Asp Ala
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Tyr Ser Ile Gly Ala Ile Thr Val Met Lys Ala Tyr Tyr Lys Gln Ser
115 120 125

Leu Ser Phe Ile Cys Gly Leu Phe Ile Val Leu Thr Thr Gln Ile Leu
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Gly Tyr Gly Trp Ala Gly Ile Leu Arg Arg Tyr Leu Val Asp Pro Val
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Asp Met Trp Trp Pro Ser Asn Leu Ala Gln Val Ser Leu Phe Arg Ala
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Leu His Glu Lys Glu Asn Lys Ser Lys Gly Leu Thr Arg Met Lys Phe
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Tyr Leu Phe Pro Ile Leu Thr Phe Ser Ser Trp Val Cys Trp Ala Trp
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Pro Asn Ser Ile Thr Ala Gln Gln Val Gly Ser Gly Tyr His Gly Leu
225 230 235 240

Gly Val Gly Ala Phe Thr Leu Asp Trp Ala Gly Ile Ser Ala Tyr His
245 250 255

Gly Ser Pro Leu Val Ala Pro Trp Ser Ser Ile Leu Asn Val Gly Val
260 265 270

Gly Phe Ile Met Phe Ile Tyr Ile Ile Val Pro Val Cys Tyr Trp Lys
275 280 285

Phe Asn Thr Phe Asp Ala Arg Lys Phe Pro Ile Ser Ser Asn Gln Leu
290 295 300

Phe Thr Thr Ser Gly Gln Lys Tyr Asp Thr Thr Lys Ile Leu Thr Pro
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Gln Phe Asp Leu Asp Ile Gly Ala Tyr Asn Asn Tyr Gly Lys Leu Tyr
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Leu Ser Pro Leu Phe Ala Leu Ser Ile Gly Ser Gly Phe Ala Arg Phe
340 345 350

Thr Ala Thr Leu Thr His Val Ala Leu Phe Asn Gly Arg Asp Ile Trp
355 360 365

Lys Gln Thr Trp Ser Ala Val Asn Thr Thr Lys Leu Asp Ile His Gly
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Lys Leu Met Gln Ser Tyr Lys Lys Val Pro Glu Trp Trp Phe Tyr Ile
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Leu Leu Ala Gly Ser Val Ala Met Ser Leu Leu Met Ser Phe Val Trp
405 410 415

Lys Glu Ser Val Gln Leu Pro Trp Trp Gly Met Leu Phe Ala Phe Ala
420 425 430

Leu Ala Phe Ile Val Thr Leu Pro Ile Gly Val Ile Gln Ala Thr Thr
435 440 445

Asn Gln Gln Pro Gly Tyr Asp Ile Ile Gly Gln Phe Ile Ile Gly Tyr
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Ile Leu Pro Gly Lys Pro Ile Ala Asn Leu Ile Phe Lys Ile Tyr Gly
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Arg Ile Ser Thr Val His Ala Leu Ser Phe Leu Ala Asp Leu Lys Leu
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Gly His Tyr Met Lys Ile Pro Pro Cys Met Tyr Thr Ala Gln Leu
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Leu Val Glu Pro Ala Ala Met Trp Trp Pro Ala Asn Leu Val Gln Val			
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325	330	335	
Pro Ile Cys Tyr Trp Leu Asp Val Tyr Lys Ala Lys Thr Phe Pro Ile			
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Ser Ile Ile Asp Ser Asn Phe His Leu Asp Leu Pro Ala Tyr Glu Arg			
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Gln Gly Pro Leu Tyr Leu Cys Thr Phe Phe Ala Ile Ser Tyr Gly Val			
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Gly Arg Glu Ile Trp Glu Gln Ser Lys Glu Ser Phe Lys Glu Lys Lys			
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Ala Cys Glu Tyr Tyr Asn Asp Gln Leu Gln Leu Pro Trp Trp Gly Val
465 470 475 480

Leu Leu Ala Cys Thr Val Ala Ile Ile Phe Thr Leu Pro Ile Gly Ile
485 490 495

Ile Thr Ala Ile Thr Asn Gln Ala Pro Gly Leu Asn Ile Ile Thr Glu
500 505 510

Tyr Ile Ile Gly Tyr Ile Tyr Pro Gly Tyr Pro Val Ala Asn Met Cys
515 520 525

Phe Lys Val Tyr Gly Tyr Ile Ser Met Gln Gln Ala Ile Thr Phe Leu
530 535 540

Gln Asp Phe Lys Leu Gly His Tyr Met Lys Ile Pro Pro Arg Thr Met
545 550 555 560

Phe Met Ala Gln Ile Val Gly Thr Leu Ile Ser Cys Phe Val Tyr Leu
565 570 575

Thr Thr Ala Trp Trp Leu Met Glu Thr Ile Pro Asn Ile Cys Asp Ser
580 585 590

Val Thr Asn Ser Val Trp Thr Cys Pro Ser Asp Lys Val Phe Tyr Asp
595 600 605

Ala Ser Val Ile Trp Gly Leu Ile Gly Pro Arg Arg Ile Phe Gly Asp
610 615 620

Leu Gly Leu Tyr Lys Ser Val Asn Trp Phe Phe Leu Val Gly Ala Ile
625 630 635 640

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Trp Ile Lys Leu Ile Asn Met Pro Val Leu Ile Ser Ala Thr Ser Ser
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Met Pro Pro Ala Thr Ala Val Asn Tyr Thr Trp Val Leu Ala Gly
675 680 685

Phe Leu Ser Gly Phe Val Val Phe Arg Tyr Arg Pro Asn Leu Trp Gln
690 695 700

Arg Tyr Asn Tyr Val Leu Ser Gly Ala Leu Asp Ala Gly Leu Ala Phe
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Met Gly Val Leu Leu Tyr Met Cys Leu Gly Leu Glu Asn Val Ser Leu
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35 40 45

Gly Ala Cys Ile Val Leu Ser Phe Ile Asn Gln Phe Phe Trp Tyr Arg
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Thr Met Pro Leu Ser Ile Thr Gly Ile Ser Ala Gln Ile Ala Val Val
65 70 75 80

Pro Leu Gly His Leu Met Ala Arg Val Leu Pro Thr Lys Arg Phe Leu
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Glu Gly Thr Arg Phe Gln Phe Thr Leu Asn Pro Gly Ala Phe Asn Val
100 105 110

Lys Glu His Val Leu Ile Thr Ile Phe Ala Asn Ser Gly Ala Gly Ser
115 120 125

Val Tyr Ala Thr His Ile Leu Ser Ala Ile Lys Leu Tyr Tyr Lys Arg
130 135 140

Ser Leu Pro Phe Leu Pro Ala Phe Leu Val Met Ile Thr Thr Gln Ile
145 150 155 160

Leu Gly Phe Gly Trp Ala Gly Leu Phe Arg Lys His Leu Val Glu Pro
165 170 175

Gly Glu Met Trp Trp Pro Ser Asn Leu Val Gln Val Ser Leu Phe Gly
180 185 190

Ala Leu His Glu Lys Glu Lys Lys Ser Arg Gly Gly Met Ser Arg Thr
195 200 205

Gln Phe Phe Leu Ile Val Leu Val Ala Ser Phe Ala Tyr Tyr Ile Phe
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Pro Gly Tyr Leu Phe Thr Met Leu Thr Ser Ile Ser Trp Val Cys Trp
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Leu Asn Pro Lys Ser Ile Leu Val Asn Gln Leu Gly Ser Gly Glu His
245 250 255

Gly Leu Gly Ile Gly Ser Ile Gly Phe Asp Trp Val Thr Ile Ser Ala
260 265 270

Tyr Leu Gly Ser Pro Leu Ala Ser Pro Leu Phe Ala Ser Val Asn Val
275 280 285

Ala Ile Gly Phe Val Leu Val Met Tyr Ile Val Thr Pro Val Cys Tyr
290 295 300

Trp Leu Asn Ile Tyr Asp Ala Lys Thr Phe Pro Ile Phe Ser Ser Gln
305 310 315 320

Leu Phe Met Gly Asn Gly Ser Arg Tyr Asp Val Leu Ser Ile Ile Asp
325 330 335

Ser Lys Phe His Leu Asp Arg Val Val Tyr Ser Arg Thr Gly Ser Ile
340 345 350

Asn Met Ser Thr Phe Phe Ala Val Thr Tyr Gly Leu Gly Phe Ala Thr
355 360 365

Leu Ser Ala Thr Ile Val His Val Leu Val Phe Asn Gly Ser Asp Leu
370 375 380

Trp Lys Gln Thr Arg Gly Ala Phe Gln Lys Asn Lys Lys Met Asp Ile
385 390 395 400

His Thr Arg Ile Met Lys Lys Asn Tyr Arg Glu Val Pro Leu Trp Trp
405 410 415

Phe Leu Val Ile Leu Leu Asn Ile Ala Leu Ile Met Phe Ile Ser
420 425 430

Val His Tyr Asn Ala Thr Val Gln Leu Pro Trp Trp Gly Val Leu Leu
435 440 445

Ala Cys Ala Ile Ala Ile Ser Phe Thr Pro Leu Ile Gly Val Ile Ala
450 455 460

Ala Thr Thr Asn Gln Ala Pro Gly Leu Asn Ile Ile Thr Glu Tyr Val
465 470 475 480

Ile Gly Tyr Ile Tyr Pro Glu Arg Pro Val Ala Asn Met Cys Phe Lys
485 490 495

Val Tyr Gly Tyr Ile Ser Met Thr Gln Ala Leu Thr Phe Ile Ser Asp
500 505 510

Phe Lys Leu Gly His Tyr Met Lys Ile Pro Pro Arg Ser Met Phe Met
515 520 525

Ala Gln Val Ala Gly Thr Leu Val Ala Val Val Val Tyr Thr Gly Thr
530 535 540

Ala Trp Trp Leu Met Glu Glu Ile Pro His Leu Cys Asp Thr Ser Leu
545 550 555 560

Leu Pro Ser Asp Ser Gln Trp Thr Cys Pro Met Asp Arg Val Phe Phe
565 570 575

Asp Ala Ser Val Ile Trp Gly Leu Val Gly Pro Arg Arg Val Phe Gly
580 585 590

Asp Leu Gly Glu Tyr Ser Asn Val Asn Trp Phe Phe Leu Val Gly Ala
595 600 605

Ile Ala Pro Leu Leu Val Trp Leu Ala Thr Lys Met Phe Pro Ala Gln

610	615	620
Thr Trp Ile Ala Lys Ile His Ile Pro Val Leu Val Gly Ala Thr Ala		
625	630	635
Met Met Pro Pro Ala Thr Ala Val Asn Phe Thr Ser Trp Leu Ile Val		
645	650	655
Ala Phe Ile Phe Gly His Phe Ile Phe Lys Tyr Arg Arg Val Trp Trp		
660	665	670
Thr Lys Tyr Asn Tyr Val Leu Ser Gly Gly Leu Asp Ala Gly Ser Ala		
675	680	685
Phe Met Thr Ile Leu Leu Phe Leu Ala Leu Gly Arg Lys Gly Ile Glu		
690	695	700
Val Gln Trp Trp Gly Asn Ser Gly Asp Arg Asp Thr Cys Pro Leu Ala		
705	710	715
Ser Cys Pro Thr Ala Lys Gly Val Val Val Lys Gly Cys Pro Val Phe		
725	730	735

<210> 7
 <211> 722
 <212> PRT
 <213> Arabidopsis thaliana

<400> 7			
Met Ala Ala Ile Glu Leu His Lys Pro Glu Ile Asn Ala Asp Asp Asp			
1	5	10	15
Asp Asp Glu Ser Pro Val Glu Gln Val Arg Leu Thr Val Ser Asn His			
20	25	30	
Asp Asp Pro Ser Leu Pro Val Trp Thr Phe Arg Met Trp Phe Leu Gly			
35	40	45	
Leu Leu Ser Cys Ile Leu Leu Ser Phe Leu Asn Thr Phe Phe Gly Tyr			
50	55	60	
Arg Thr Gln Pro Leu Met Ile Thr Met Ile Ser Val Gln Val Val Thr			
65	70	75	80
Leu Pro Leu Gly Lys Leu Met Ala Arg Val Leu Pro Glu Thr Lys Tyr			
85	90	95	
Lys Ile Gly Ser Trp Glu Phe Ser Phe Asn Pro Gly Pro Phe Asn Val			
100	105	110	
Lys Glu His Val Leu Ile Ser Met Phe Ala Asn Ala Gly Ala Gly Phe			
115	120	125	
Gly Ser Gly Thr Ala Tyr Ala Val Gly Ile Val Asp Ile Ile Met Ala			
130	135	140	
Phe Tyr Lys Arg Lys Ile Ser Phe Leu Ala Ser Trp Ile Leu Val Ile			
145	150	155	160
Thr Thr Gln Asp Asn Ala Arg Met Ser Arg Gly Lys Phe Phe Val Ile			

	165	170	175
Ala Phe Val Cys Ser Phe Ala Trp Tyr Ile Phe Pro Ala Tyr Leu Phe			
180	185		190
Leu Thr Leu Ser Ser Ile Ser Trp Val Cys Trp Ala Phe Pro Lys Ser			
195	200		205
Ile Thr Ala Gln Gln Leu Gly Ser Gly Met Ser Gly Leu Gly Ile Gly			
210	215		220
Ala Phe Ala Leu Asp Trp Ser Val Ile Ala Ser Tyr Leu Gly Ser Pro			
225	230	235	240
Leu Val Thr Pro Phe Phe Ala Ile Val Asn Val Leu Val Gly Tyr Val			
245	250		255
Leu Val Met Tyr Met Val Ile Pro Ile Ser Tyr Trp Gly Met Asn Val			
260	265		270
Tyr Glu Ala Asn Lys Phe Pro Ile Phe Ser Ser Asp Leu Phe Asp Lys			
275	280		285
Gln Gly Gln Leu Tyr Asn Ile Ser Thr Ile Val Asn Asn Lys Phe Glu			
290	295		300
Leu Asp Met Glu Asn Tyr Gln Gln Gln Gly Arg Val Tyr Leu Ser Thr			
305	310	315	320
Phe Phe Ala Ile Ser Tyr Gly Ile Gly Phe Ala Ala Ile Val Ser Thr			
325	330		335
Leu Thr His Val Ala Leu Phe Asn Gly Lys Gly Ile Trp Gln Gln Val			
340	345		350
Arg Ala Ser Thr Lys Ala Lys Met Asp Ile His Thr Arg Leu Met Lys			
355	360		365
Lys Tyr Lys Asp Ile Pro Gly Trp Trp Phe Tyr Ser Leu Leu Ala Ile			
370	375		380
Ser Leu Val Leu Ser Leu Val Leu Cys Ile Phe Met Lys Asp Glu Ile			
385	390	395	400
Gln Met Pro Trp Trp Gly Leu Leu Leu Ala Ser Phe Met Ala Leu Thr			
405	410		415
Phe Thr Val Pro Val Ser Ile Ile Thr Ala Thr Thr Asn Gln Thr Pro			
420	425		430
Gly Leu Asn Ile Ile Thr Glu Tyr Leu Met Gly Val Leu Leu Pro Gly			
435	440		445
Arg Pro Ile Ala Asn Val Cys Phe Lys Thr Tyr Gly Tyr Ile Ser Met			
450	455		460
Ser Gln Ala Ile Ser Phe Leu Asn Asp Phe Lys Leu Gly His Tyr Met			
465	470	475	480
Lys Ile Pro Pro Arg Ser Met Phe Leu Val Gln Phe Ile Gly Thr Val			
485	490		495

Ile Ala Gly Thr Val Asn Ile Ser Val Ala Trp Tyr Leu Leu Thr Ser
500 505 510

Val Glu Asn Ile Cys Gln Lys Glu Leu Leu Pro Pro Asn Ser Pro Trp
515 520 525

Thr Cys Pro Ser Asp Arg Val Phe Phe Asp Ala Ser Val Ile Trp Gly
530 535 540

Leu Val Gly Pro Lys Arg Ile Phe Gly Arg Leu Gly Asn Tyr Pro Ala
545 550 555 560

Leu Asn Trp Phe Phe Leu Gly Gly Leu Ile Gly Pro Val Leu Val Trp
565 570 575

Leu Leu Gln Lys Ala Phe Pro Thr Lys Thr Trp Ile Ser Gln Ile Asn
580 585 590

Leu Pro Val Leu Leu Gly Ala Thr Ala Ala Met Pro Pro Ala Thr Ser
595 600 605

Val Asn Phe Asn Cys Trp Ile Ile Val Gly Val Ile Phe Asn Tyr Phe
610 615 620

Val Phe Lys Tyr Cys Lys Lys Trp Trp Gln Arg Tyr Asn Tyr Val Leu
625 630 635 640

Ser Ala Ala Leu Asp Ala Gly Leu Ala Phe Met Gly Val Leu Leu Tyr
645 650 655

Phe Ser Leu Thr Met Asn Gly Ile Ser Ile Asn His Trp Trp Gly Ala
660 665 670

Lys Gly Glu Asn Cys Pro Leu Ala Ser Cys Pro Thr Ala Pro Gly Val
675 680 685

Leu Val Asp Asp Phe Thr Val Phe Phe Phe Leu Lys Ile Phe Val
690 695 700

Pro Phe Val Asn Lys Asn Arg Leu Asn Asp Phe Leu Ser Met Tyr Leu
705 710 715 720

Leu Tyr

<210> 8
<211> 783
<212> PRT
<213> Candida albicans

<400> 8
Met Asp Lys Ile Arg Ala Val Ile Ser Gly Gly Glu Lys Pro Pro Val
1 5 10 15

Asp Thr Asp Asn Asp His Asn Thr Asp Phe Glu Ala Asp Arg Lys Met
20 25 30

Pro Asp Leu Asp Ile Val Val Ser Lys Ser Gln Glu Phe Asp Pro Val
35 40 45

Thr Ser His Leu Val Asn Asp Ile Met Glu Asp Glu Tyr Ala Ala Val
50 55 60

His Val Glu Asp Asp Ser Pro Tyr Pro Glu Val Arg Ala Ala Val Pro
65 70 75 80

Ser Thr Asp Asp Pro Thr Leu Pro Gln Asn Thr Ile Arg Ala Trp Val
85 90 95

Ile Gly Leu Ile Leu Thr Thr Val Gly Cys Gly Met Asn Met Leu Phe
100 105 110

Ser Phe His Ser Pro Ser Phe Ala Ile Thr Thr Phe Val Thr Ser Ile
115 120 125

Leu Ala Trp Pro Ile Gly Asn Phe Trp Ala Trp Ile Val Pro Asp Trp
130 135 140

Lys Ile Phe Gly Ala Ser Leu Asn Pro Gly Pro Phe Asn Val Lys Glu
145 150 155 160

His Thr Ile Ile Thr Ile Met Ala Asn Val Ser Phe Gly Thr Gly Ala
165 170 175

Ala Thr Ala Thr Asp Ile Leu Leu Ala Gln Asn Met Phe Tyr Lys Ser
180 185 190

Asn Phe Gly Trp Gly Tyr Asn Leu Leu Leu Ile Trp Ser Thr Gln Cys
195 200 205

Ile Gly Phe Ala Phe Gly Gly Val Met Arg Arg Phe Val Val Asp Ser
210 215 220

Pro Gly Ala Ile Trp Pro Ser Asn Leu Val Thr Ala Thr Phe Leu Thr
225 230 235 240

Asn Met His Ile Asn Glu Asn His Thr Ala Asn Gly Trp Lys Ile Ser
245 250 255

Arg Leu Ala Phe Phe Val Ile Val Phe Val Ala Ser Phe Val Trp Tyr
260 265 270

Trp Phe Pro Gly Tyr Ile Phe Gln Ala Leu Ser Tyr Phe Ser Trp Ile
275 280 285

Thr Trp Ile Lys Pro Asn Asn Val Ile Ile Asn Gln Val Phe Gly Ser
290 295 300

Ser Ser Gly Leu Gly Met Ile Pro Asn Asn Ile Ala Leu Asp Trp Asn
305 310 315 320

Gln Ile Ala Gly Tyr Ile Gly Ser Pro Leu Ile Pro Pro Ala Ser Val
325 330 335

Ile Ala Thr Ile Phe Gly Ser Ile Val Leu Ile Phe Trp Ile Val Val
340 345 350

Pro Ala Ile His Tyr Ser Asn Thr Trp Tyr Ser Gln Tyr Leu Pro Ile
355 360 365

Ser Ser Thr Gly Ser Phe Asp Arg Phe Gln Gln Thr Tyr Asn Val Ser
370 375 380

Lys Ile Ile Asp His Lys Thr Leu Ser Phe Asn Glu Ala Glu Tyr Lys
385 390 395 400

Lys Tyr Ser Pro Leu Phe Leu Ser Thr Thr Phe Ala Ile Ser Tyr Gly
405 410 415

Leu Ser Phe Ala Ser Ile Leu Ala Thr Ile Thr His Thr Ile Cys Phe
420 425 430

His Gly Arg Asp Leu Ile Ala Ser Leu Lys Ala Lys Glu Lys Pro Asp
435 440 445

Val His Asn Arg Leu Met Lys Ala Tyr Lys Pro Val Pro Glu Trp Trp
450 455 460

Tyr Leu Val Val Phe Leu Val Phe Phe Gly Met Ser Ile Ala Thr Val
465 470 475 480

Arg Ala Trp Pro Thr Glu Met Pro Val Trp Gly Leu Val Phe Ala Leu
485 490 495

Ile Ile Ala Ile Ile Phe Leu Leu Pro Val Ala Ile Ile Tyr Ala Lys
500 505 510

Thr Asn Ile Ala Val Gly Leu Asn Val Val Thr Glu Phe Ile Val Gly
515 520 525

Tyr Val Leu Gly Gly Arg Pro Leu Cys Met Met Leu Phe Lys Thr Phe
530 535 540

Gly Tyr Ile Thr Asn Asn Gln Ala Val Thr Phe Val Gln Asp Met Lys
545 550 555 560

Leu Gly His Tyr Met Lys Ile Asp Pro Arg Thr Leu Phe Trp Ala Gln
565 570 575

Phe Ala Ala Thr Ile Trp Gly Ser Leu Val Gln Ile Ala Val Leu Glu
580 585 590

Trp Ala Tyr Gly Ala Ile Asp Asn Leu Cys Ala Ala Asp Gln Lys Asn
595 600 605

His Tyr Thr Cys Pro Asn Gly Lys Val Phe Phe Asn Ala Ser Ile Ile
610 615 620

Trp Gly Val Ile Gly Pro Gln Arg Gln Phe Ser His Gly Gln Ile Tyr
625 630 635 640

Tyr Gly Leu Leu Phe Phe Ile Ile Gly Ala Val Thr Pro Val Ile
645 650 655

Asn Trp Leu Ile Leu Lys Lys Trp Pro Asn Ser Pro Val Lys Tyr Leu
660 665 670

His Trp Pro Val Phe Phe Ser Gly Thr Gly Tyr Ile Pro Pro Ala Thr
675 680 685

Pro Tyr Asn Tyr Thr Ser Tyr Cys Ala Val Gly Leu Phe Phe Gly Trp

690	695	700
Trp Ile Lys Lys Trp Phe His Trp Trp Ser Lys Tyr Asn Tyr Ser		
705	710	715
Leu Ser Ala Gly Leu Asp Ile Gly Leu Ala Trp Cys Ser Leu Ile Ile		
725	730	735
Phe Leu Cys Leu Ser Leu Thr Asn Thr Asp Phe Pro Ser Trp Trp Gly		
740	745	750
Asn Asp Val Ile Asn Thr Thr Leu Asp Thr Gln Val Val Thr Asn Ile		
755	760	765
Arg His Ile Leu Lys Glu Gly Glu Ala Phe Gly Pro Ser Ser Trp		
770	775	780

<210> 9
<211> 877
<212> PRT
<213> *Saccharomyces cerevisiae*

<400> 9		
Met Ser Glu Thr Val Lys Asp Lys Val Ile Ile Asp Glu Lys Val Ser		
1	5	10
Thr Lys Gly Thr Val Asp Tyr Ala Glu Gly Ala Glu Tyr Ser Glu Arg		
20	25	30
Leu Ser Asn His Ser Ser Asp Phe Ser Gln Trp Tyr Thr Asp Glu Gln		
35	40	45
Ile Leu His Phe Met Lys Lys Leu Gly Tyr Glu Asn Arg Thr Leu Tyr		
50	55	60
Asp Ile Pro Glu Asp Val Ala Tyr Ile Leu Lys Lys Met Pro Glu Leu		
65	70	75
Thr Leu Glu Asp Ser Phe Lys Ile Leu Lys Asp Ser Ile Ile Tyr Phe		
85	90	95
Lys Asp Asp Glu Asn Ile Pro His Asp Gln Tyr Glu Glu Trp Lys Arg		
100	105	110
Leu Val Asp Leu Glu Asp Leu Asp Ser Lys Glu Gly Ile Asp Glu Tyr		
115	120	125
Asp Ser Phe Asp Ile Arg Ala Phe Ala Ser Ala Ile Lys Phe His Ser		
130	135	140
Pro Tyr Gln Glu Val Arg Ala Val Val Asp Pro Glu Asp Asp Pro Thr		
145	150	155
Ile Pro Val Glu Thr Phe Arg Ala Tyr Phe Leu Ala Ile Ile Trp Ser		
165	170	175
Val Ile Gly Ser Gly Phe Asn Glu Phe Phe Ser His Arg Val Val Ser		
180	185	190
Ile Ser Leu Asn Thr Pro Ile Ile Gln Met Phe Leu Tyr Ile Cys Gly		

195 200 205
Lys Ala Trp Ala Lys Thr Ile Pro Cys Trp Thr Ile Thr Ile Arg Gly
210 215 220
Arg Lys Tyr Gly Ile Asn Ile Asp Lys Pro Trp Thr Gln Lys Glu Gln
225 230 235 240
Met Phe Ser Thr Leu Leu Tyr Ala Ile Cys Gln Gly Ala Phe Tyr Thr
245 250 255
His Tyr Asn Ile Leu Thr Gln Lys Leu Phe Tyr His Ser Ala Phe Ser
260 265 270
Phe Gly Tyr Gln Phe Leu Leu Ser Leu Ser Val Gln Phe Ile Gly Phe
275 280 285
Gly Phe Ala Gly Ile Leu Arg Lys Phe Val Val Tyr Pro Ala Arg Ala
290 295 300
Leu Trp Pro Thr Val Met Pro Thr Ile Ala Ile Asn Lys Ala Leu Leu
305 310 315 320
Gly Lys Glu Lys His Glu Ser Gly Met Ser Arg Tyr Lys Phe Phe Phe
325 330 335
Leu Thr Phe Phe Ile Met Phe Ile Tyr Asn Trp Phe Pro Thr Tyr Ile
340 345 350
Ile Asn Ile Leu Asn Thr Phe Asn Trp Met Thr Trp Ile Lys Pro Ser
355 360 365
Asn Ile Asn Leu Ala Asn Ile Thr Gly Gly Val Thr Gly Leu Gly Ile
370 375 380
Asn Pro Ile Ser Ser Phe Asp Trp Asn Val Ile Ser Phe Asn Ser Pro
385 390 395 400
Leu Val Tyr Pro Phe Trp Ser Tyr Leu Thr Gln Tyr Leu Gly Cys Ile
405 410 415
Leu Ala Ala Leu Ile Val Ile Ala Val Tyr Tyr Ser Asn Tyr Met Ser
420 425 430
Cys Gln Tyr Leu Pro Ile Phe Thr Asn Ser Leu Tyr Thr Asn Thr Gly
435 440 445
His Ser Phe Lys Val Thr Glu Val Leu Asp Ser Asp Asn Lys Leu Asp
450 455 460
Val Lys Lys Tyr Gln Ser Tyr Ser Pro Pro Tyr Tyr Ser Ala Gly Asn
465 470 475 480
Leu Val Ser Tyr Gly Ala Phe Ile Cys Ala Tyr Pro Leu Met Ile Thr
485 490 495
Trp Ser Phe Ile Val His Ser Lys Leu Leu Phe Asn Ala Phe Lys Asp
500 505 510
Trp Ala Leu Asn Leu Trp Ala Met Arg Lys Leu Lys Ser Trp Val Thr
515 520 525

Met Phe Lys Ser Asp Tyr Arg Ala Leu Asp Asp Tyr Asp Asp Pro His
530 535 540

Ser Asn Ala Met Lys Asn Tyr Lys Glu Val Pro Asp Trp Trp Tyr Phe
545 550 555 560

Ala Ile Leu Ile Gly Ser Leu Val Val Gly Ile Ala Val Val Glu His
565 570 575

Tyr Pro Thr Asn Thr Pro Val Trp Gly Leu Phe Val Cys Leu Gly Phe
580 585 590

Asn Phe Val Phe Leu Ile Pro Thr Thr Ile Leu Gln Ala Thr Thr Gly
595 600 605

Tyr Ser Phe Gly Leu Asn Leu Ile Glu Met Val Met Gly Tyr Ala
610 615 620

Leu Pro Gly Asn Pro Ile Ala Ile Met Ile Leu Lys Ala Phe Gly Tyr
625 630 635 640

Asn Ile Asp Gly Gln Ala Asp Asn Tyr Val Ser Asn Leu Lys Ile Ala
645 650 655

His Tyr Cys Lys Ile Pro Pro Met Ala Leu Phe Arg Gly Gln Cys Val
660 665 670

Ile Val Phe Ile Gln Ile Phe Val Asn Leu Gly Val Leu Asn Trp Gln
675 680 685

Ile Ser Asn Ile Lys Asp Phe Cys Thr Pro His Gln Asn Ala Lys Phe
690 695 700

Thr Cys Pro Asp Ala Val Thr Tyr Tyr Asn Ala Ser Val Val Trp Gly
705 710 715 720

Ala Ile Gly Pro Lys Arg Ile Phe Asn Tyr Ile Tyr Pro Ile Phe Lys
725 730 735

Trp Cys Trp Leu Ile Gly Ala Cys Ile Gly Ile Phe Phe Gly Val Trp
740 745 750

Lys Arg Trp Gly Lys Phe Tyr Pro Arg Tyr Phe Asp Pro Met Leu Phe
755 760 765

Val Gly Gly Met Leu Asn Met Ser Pro Pro Tyr Asn Leu Met Tyr Tyr
770 775 780

Thr Ser Gly Met Ile Val Ser Tyr Ile Ser Gln Tyr Tyr Met Lys Arg
785 790 795 800

His His Leu Asn Leu Trp Glu Lys Tyr Asn Tyr Val Leu Ser Ala Gly
805 810 815

Phe Ser Thr Gly Leu Val Leu Ser Ala Ile Ile Ile Phe Phe Ala Val
820 825 830

Gln Tyr Lys Asp Thr Ala Phe Asn Trp Trp Gly Asn Thr Val Pro Tyr
835 840 845

Ala Gly Ala Asp Gly Val Gly Tyr Pro Leu Lys Asn Ile Thr Asp Thr
850 855 860

Ala Asn Gly Tyr Phe Gly Tyr Ala Pro Gly His Tyr Pro
865 870 875

<210> 10
<211> 851
<212> PRT
<213> Schizosaccharomyces pombe

<400> 10
Met Thr Ala Arg Asn Ser Ala Ser Ile Pro Thr Ser Ile Arg Lys Thr
1 5 10 15

Ser Glu Asn Glu Val Ser Gly Asp Glu Thr Pro Ala Gly Val Gly Asn
20 25 30

Leu Ser Thr Lys Thr Ala Ser Lys Thr Ser Leu Thr Phe Arg Gln Ser
35 40 45

Ser Ser Asp Glu Ser Thr Ser Ser Tyr Ser Gly Asn His His Asn Ile
50 55 60

Asn Ile Gln His His Pro Asn Arg Pro Phe Arg Thr Asn Ser Ser Ser
65 70 75 80

Phe Ser Pro Asn Asp Tyr Ser Ile Ser Glu Ser Pro Ser Lys Ser Lys
85 90 95

Lys Asp Gly Val His Val Ser Ala Val Gln Leu Asp Asn Glu Thr Asp
100 105 110

Ser Glu Val Glu Ser Glu Val Glu Glu Leu Glu Arg Glu Leu Glu Ala
115 120 125

Ile Glu Asp Ser Val Tyr Pro Glu Val Arg Ala Ala Val Asn Pro Thr
130 135 140

Asp Asp Val Asn Leu Pro Val Asn Thr Trp Arg Thr Trp Val Leu Thr
145 150 155 160

Thr Ile Phe Val Ile Val Phe Ala Ala Val Asn Gln Phe Phe Ser Leu
165 170 175

Arg Tyr Pro Ala Leu Ser Ile Ser Phe Ile Val Ala Gln Leu Ile Leu
180 185 190

Phe Pro Leu Gly Lys Leu Leu Asn Leu Leu Pro Asn Trp Lys Ile Gly
195 200 205

Tyr Gly Arg Phe Ser Phe Tyr Leu Asn Ser Ser Pro Phe Asn Val Lys
210 215 220

Glu His Ala Ala Ile Thr Ile Ala Val Ser Leu Thr Ser Ser Thr Ala
225 230 235 240

Tyr Ala Thr Asn Ile Leu Ser Ala Gln Thr Ser Phe Tyr Lys Gln Asn
245 250 255

Leu Ser Trp Gly Tyr Lys Ile Leu Ile Val Leu Thr Ser Gln Met Leu
260 265 270

Gly Tyr Gly Phe Ala Gly Leu Thr Arg Arg Trp Ile Val Tyr Pro Ala
275 280 285

Ala Met Ile Trp Pro Gln Thr Leu Val Ser Thr Val Leu Phe Arg Thr
290 295 300

Leu His Gly Asn Ser Gly Asn Asp Ile Gly Val Leu Lys Asn Asn Arg
305 310 315 320

Ile Ser Ala Asn Gly Trp Thr Ile Ser Arg Tyr Arg Phe Phe Ala Tyr
325 330 335

Val Met Ile Gly Ser Phe Val Phe Tyr Trp Phe Pro Gly Phe Ile Phe
340 345 350

Lys Gly Leu Ser Tyr Phe Thr Val Leu Cys Trp Ile Trp Pro Lys Asn
355 360 365

Arg Val Val Asn Gln Leu Phe Gly Tyr Asn Ser Gly Leu Gly Ile Leu
370 375 380

Pro Leu Thr Phe Asp Trp Gln Gln Val Val Tyr Asn Ser Asn Pro Leu
385 ~ 390 395 400

Ala Ser Pro Trp Trp Val Ile Cys Asn Thr Phe Gly Ser Val Val Leu
405 410 415

Ile Phe Trp Ile Val Val Pro Ile Leu Tyr Tyr Lys Gly Val Trp Phe
420 425 430

Ser Asn Tyr Leu Pro Met Leu Ser Ser Ser Thr Phe Asp His Thr Gly
435 440 445

Val Ser Tyr Asn Ser Ser Arg Val Leu Asn Ser Asp Tyr Ser Phe Asn
450 455 460

His Thr Lys Tyr Glu Ser Tyr Ser Pro Leu Tyr Met Pro Met Ser Tyr
465 470 475 480

Ser Met Ser Thr Ala Leu Asn Phe Ala Ala Val Thr Ala Ile Phe Thr
485 490 495

His Cys Ala Leu Tyr Asn Gly Lys Asp Ile Trp Gln Arg Leu Trp Lys
500 505 510

Glu Ser Gly Lys Asp Glu Cys Ile His Arg Lys Leu Met Arg Asn Tyr
515 520 525

Lys Glu Ala Pro Gln Trp Trp Tyr Ala Thr Leu Phe Ile Val Val Phe
530 535 540

Gly Leu Thr Ile Phe Thr Val Arg Tyr Tyr Asp Thr Gln Cys Pro Val
545 550 555 560

Trp Ala Leu Ile Val Ala Leu Leu Ile Phe Ile Val Asn Phe Ile Pro
565 570 575

Gln Gly Val Leu Glu Gly Ile Thr Asn Gln His Val Gly Leu Asn Ile

580	585	590	
Ile Thr Glu Leu Ile Gly Gly Tyr Ile Leu Pro Gly Lys Pro Leu Ala			
595	600	605	
Asn Leu Met Ile Lys Leu Tyr Gly Phe Ile Pro Met Arg Gln Gly Leu			
610	615	620	
Glu Phe Ser Arg Asp Leu Lys Leu Ala Gln Tyr Met Lys Ile Pro Pro			
625	630	635	640
Arg Ile Leu Phe Phe Val Gln Leu Phe Ala Thr Ile Leu Gly Gly Ile			
645	650	655	
Thr Gln Val Ala Val Gln Glu Trp Met Asn Tyr His Ile Pro Gly Ile			
660	665	670	
Cys Thr Thr Ser Gln Ser Asn Gly Phe Thr Cys Pro Asn Gly Arg Ser			
675	680	685	
Ile Tyr Asn Ala Ser Leu Ile Trp Gly Ala Ile Gly Pro Ala Lys Met			
690	695	700	
Phe Ser Lys Gly Lys Pro Tyr Tyr Pro Leu Ile Phe Phe Phe Leu Ile			
705	710	715	720
Gly Ala Val Ala Pro Phe Ile Thr Trp Gly Leu Arg Lys Arg Phe Pro			
725	730	735	
Lys Ser Trp Ile Gly Lys Leu Asn Ala Pro Val Leu Phe Thr Gly Pro			
740	745	750	
Gly Asn Ile Pro Pro Ala Thr Gly Ile Asn Tyr Ser Ser Trp Ala Ile			
755	760	765	
Val Gly Phe Ile Phe Asn Tyr Val Ile Arg Lys Arg Ala Ile His Trp			
770	775	780	
Trp Arg Lys Tyr Asn Tyr Val Leu Ala Ala Ala Met Asp Ser Gly Val			
785	790	795	800
Ala Val Ala Gly Val Val Ile Phe Leu Cys Val Ser Tyr Pro Gly Gly			
805	810	815	
Lys Ile Thr Trp Trp Gly Asn Thr Val Tyr Thr Lys Thr Tyr Asp Trp			
820	825	830	
Lys Ser Val Pro Tyr Arg Ser Leu Gly Pro Asn Glu Thr Phe Gly Tyr			
835	840	845	
Thr Asn Trp			
850			

<210> 11
<211> 791
<212> PRT
<213> Schizosaccharomyces pombe

<400> 11
Met Lys Thr Pro Lys Phe Ile Thr Tyr Val Thr Arg Gly Phe Lys Gly

1	5	10	15
Leu	Glu	Ser	Lys
20	25	30	
Ser	Ser	Pro	Ile
35	40	45	
Ser	Phe	Glu	Ile
50	55	60	
Ile	Thr	Glu	Arg
65	70	75	80
Thr	Val	Arg	Asp
85	90	95	
Ile	Pro	Ala	Ser
100	105	110	
Thr	Val	Ile	Ala
115	120	125	
Val	Ser	Ile	Ala
130	135	140	
Gln	Leu	Trp	Tyr
145	150	155	160
Gly	Ile	Arg	Val
165	170	175	
Ala	Cys	Leu	Tyr
180	185	190	
Asn	Thr	Leu	Ile
195	200	205	
Ile	Gly	Arg	Ala
210	215	220	
Gly	Trp	Ser	Gly
225	230	235	240
Ile	Trp	Pro	Ser
245	250	255	
Asp	Asn	Asp	Asn
260	265	270	
Tyr	Phe	Phe	Ile
275	280	285	
Asp	Leu	Ile	Phe
290	295	300	
Cys	Lys	Pro	Ser
305	310	315	320
Gly	Leu	Gly	Leu
325	330	335	

Leu Ser Asn Pro Leu Ile Thr Pro Trp Trp Ala Thr Cys Cys Ile Phe
340 345 350

Thr Ser Phe Val Phe Trp Ile Trp Ile Val Leu Pro Gly Leu Tyr Tyr
355 360 365

Gln Asn Tyr Trp Gln Val Ala His Phe Pro Ile Met Thr Asn Ser Ile
370 375 380

Tyr Thr Val Ser Gly Lys Ser Tyr Asp Ala Gln Lys Val Val Asp Ser
385 390 395 400

Lys Trp Glu Leu Val Thr Gln Lys Tyr Gln Glu Tyr Ser Pro Val Met
405 410 415

Leu Pro Ile Ala Phe Ile Ile Asn Ile Ala Leu Ser Leu Gly Ala Phe
420 425 430

Ser Ser Met Met Ile Ser Phe Phe Leu Arg Phe Pro Thr Asp Val Ile
435 440 445

Gln Pro Ile Cys His Val Phe Lys Tyr Ser Asp Ile His Thr Lys Leu
450 455 460

Leu Lys Lys Tyr Lys Arg Val His Trp Gly Phe Tyr Leu Ala Ser Ile
465 470 475 480

Ile Val Ser Leu Gly Leu Gly Phe Ala Phe Thr Glu Gly Trp His Asp
485 490 495

Ile Gln Ile Arg Ser Tyr Gly Phe Val Val Ser Met Val Ile Gly Ala
500 505 510

Ala Leu Tyr Ile Pro Leu Ser Leu Ile Glu Ser Arg Ser Ser Phe Thr
515 520 525

Ile Ser Met Gln Ala Phe Phe Glu Ile Val Ala Ala Phe Trp Phe Asn
530 535 540

Gly Gln Pro Met Ala Leu Leu Tyr Phe Tyr Ser Phe Gly Phe Gly Thr
545 550 555 560

Leu Gln His Ala Met His Met Thr Gln Ser Ala Lys Ile Gly His Tyr
565 570 575

Met Lys Val Pro Pro Arg Leu Val Ala Ala Leu Leu Phe Thr Ser Gly
580 585 590

Ile Trp Ser Ser Leu Val Asn Ser Ala Val Thr Gly Trp Ile Met Tyr
595 600 605

His Val Arg Asp Val Cys Thr Ser Asn Ala Glu Asn Asn Met Thr Cys
610 615 620

Arg Ser Pro Lys Thr Gln Phe Asn Ser His Leu Ile Trp Gly Leu Val
625 630 635 640

Gly Asn His Ile Phe Ser Ser Asp Gly Arg Tyr Ser Phe Val Met Trp
645 650 655

Phe Phe Leu Val Gly Ala Val Val Ser Val Val Val Tyr Leu Leu Gln
 660 665 670
 Ile Ser Phe Pro Lys Ser Ser Trp Lys His Val Asn Pro Ala Leu Leu
 675 680 685
 Leu Gly Gly Ala Ala Gln Ile Pro Ser Val Thr Gly Ile Asn Tyr Ser
 690 695 700
 Thr Trp Ala Ala Val Ala Phe Cys Phe Asn Tyr Leu Ile Arg Arg Gly
 705 710 715 720
 Tyr Tyr Ser Trp Trp Lys Lys Tyr Asn Leu Ile Thr Ala Ala Met
 725 730 735
 Asp Cys Gly Val Ala Ile Ala Gly Leu Phe Ile Tyr Phe Cys Val Val
 740 745 750
 Tyr Thr Gly Gly Ser Ser Asn Phe Ser Trp Trp Gly Thr Thr Val Ser
 755 760 765
 Ser Ala Gly Cys Asp Lys Lys Gly Cys Ala His Leu Ser Val Ser Asp
 770 775 780
 Ile Ser Lys Pro Ser Gly Trp
 785 790

<210> 12
 <211> 776
 <212> PRT
 <213> Schizosaccharomyces pombe

<400> 12
 Met Ile Gly Ser Ile Asn Glu Ser Pro Ile Glu Glu His Met Asn Asp
 1 5 10 15
 Ser Pro Ser Thr Lys Glu Lys Ala Asp Ser Val Asp Ile Ser Asp Tyr
 20 25 30
 Ile Val Ser His Ser Asp Asp Ser Leu Ser Lys Asp Ile Lys Lys Asp
 35 40 45
 Thr Lys Ser Phe Leu Asp Val Glu His Gly Glu Ile Ser Thr Val Asp
 50 55 60
 Glu Phe Glu Glu Asp Ser Pro Tyr Pro Glu Val Arg Ala Ala Val Pro
 65 70 75 80
 Pro Thr Asp Asp Pro Ser Met Pro Cys Asn Thr Ile Arg Met Trp Thr
 85 90 95
 Ile Gly Leu Ile Tyr Ser Thr Val Gly Ala Ala Val Asn Met Phe Phe
 100 105 110
 Ser Leu Arg Asn Pro Thr Val Thr Leu Ser Val Leu Ile Ser Glu Leu
 115 120 125
 Leu Ala Tyr Pro Ala Leu Gln Ile Trp Asp Leu Ile Phe Pro Asp Arg
 130 135 140

Glu Phe Arg Ile Gly Arg Leu Lys Phe Asn Phe Lys Pro Gly Pro Phe
145 150 155 160

Asn Val Lys Glu His Ala Leu Ile Val Val Met Ser Ser Val Ser Phe
165 170 175

Gly Asn Ala Tyr Ser Thr Asp Ile Ile Leu Ala Gln Arg Val His Tyr
180 185 190

Lys Gln Arg Phe Gly Phe Gly Tyr Glu Ile Cys Leu Thr Leu Ala Thr
195 200 205

Gln Leu Ile Gly Tyr Gly Leu Ala Gly Leu Ser Arg Arg Leu Leu Val
210 215 220

Arg Pro Ala Ser Met Leu Trp Pro Val Asn Leu Val Gln Cys Thr Leu
225 230 235 240

Ile Lys Thr Leu His Arg Lys Asp Leu Arg Asn Ala Val Ala Asn Gly
245 250 255

Trp Arg Ile Ser Pro Phe Arg Phe Phe Leu Tyr Val Phe Ile Ala Ser
260 265 270

Phe Ile Trp Asn Trp Phe Pro Ser Tyr Ile Phe Gln Ala Leu Ser Leu
275 280 285

Phe Ala Trp Val Thr Trp Ile Arg Pro Asn Ser Pro Thr Val Asn Gln
290 295 300

Ile Phe Gly Glu Ser Thr Gly Ile Ser Ile Leu Pro Met Thr Phe Asp
305 310 315 320

Trp Asn Gln Ile Ser Ala Tyr Ile Leu Ser Pro Leu Met Ala Pro Ala
325 330 335

Asp Ala Leu Met Asn Ile Leu Leu Gly Val Ile Leu Phe Phe Trp Ile
340 345 350

Val Thr Pro Ala Leu Asn Phe Thr Asn Thr Trp Tyr Gly Asp Tyr Leu
355 360 365

Pro Ile Ser Ser Ser Gly Ile Ile Asp His Phe Gly Asn Ser Tyr Asn
370 375 380

Val Thr Arg Ile Leu Thr Lys Asp Ala Thr Phe Asp Leu Asp Ala Tyr
385 390 395 400

Gln Asn Tyr Ser Pro Ile Phe Met Ser Thr Thr Tyr Ala Leu Ala Phe
405 410 415

Gly Leu Ser Phe Ala Ser Ile Thr Ser Val Ile Phe His Val Ile Leu
420 425 430

Tyr His Gly Lys Glu Ile Tyr Asp Arg Leu Arg Asp Pro Pro Ala Pro
435 440 445

Asp Ile His Glu Lys Leu Met Lys Ala Tyr Asp Glu Val Pro Phe Tyr
450 455 460

Trp Tyr Leu Ser Val Phe Leu Ala Phe Phe Gly Met Met Met Gly Thr

465	470	475	480
Ile Tyr Gly Trp Lys Thr Glu Thr Pro Trp Trp Val Ile Ile Val Gly			
485	490	495	
Val Ile Phe Ser Ala Val Trp Phe Ile Pro Ile Gly Ile Val Gln Ala			
500	505	510	
Ile Thr Asn Ile Gln Leu Gly Leu Asn Val Phe Thr Glu Phe Ile Val			
515	520	525	
Gly Tyr Met Tyr Pro Gly Arg Pro Leu Ala Met Met Ile Phe Lys Thr			
530	535	540	
Val Gly Tyr Ile Thr Met Thr Gln Gly Leu Ala Phe Ala Ala Asp Leu			
545	550	555	560
Lys Glu Gly His Tyr Met Lys Leu Pro Pro Arg Ile Met Phe Tyr Thr			
565	570	575	
Gln Met Ile Ala Thr Ile Trp Ser Cys Phe Val Gln Ile Gly Val Leu			
580	585	590	
Asp Trp Ala Leu Gly Asn Ile Asp Asn Val Cys Gln Ala Asp Gln Pro			
595	600	605	
Asp Asn Tyr Thr Cys Pro Asn Ala Thr Val Phe Phe Asn Ser Ser Val			
610	615	620	
Ile Trp Gly Val Ile Gly Pro Lys Arg Met Phe Ser Gly Lys Asn Thr			
625	630	635	640
Tyr Thr Gly Leu Gln Tyr Phe Trp Leu Ala Gly Val Leu Gly Thr Ile			
645	650	655	
Leu Phe Trp Ala Leu Trp Lys Lys Trp Pro Gln Lys Trp Trp Gly Gln			
660	665	670	
Leu Asn Gly Pro Leu Ile Phe Gly Gly Thr Gly Tyr Ile Pro Pro Ala			
675	680	685	
Thr Pro Val Asn Tyr Leu Ala Trp Ser Gly Ile Gly Leu Phe Phe Asn			
690	695	700	
Tyr Tyr Leu Lys Lys Ile Phe Ala Asp Trp Trp Gln Lys Tyr Asn Phe			
705	710	715	720
Thr Leu Ser Ala Leu Asp Thr Gly Thr Gln Leu Ser Val Ile Ile Leu			
725	730	735	
Phe Phe Cys Leu Gln Leu Pro Met Val Asn Phe Pro Asp Trp Trp Gly			
740	745	750	
Asn Asp Gly Ala Phe Asn Thr Leu Asp Ala Thr Gly Ala Ala Val Arg			
755	760	765	
Lys Leu Val Asn Glu Ser Ala Arg			
770	775		

<211> 776
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: Isp4

<400> 13

Met	Ile	Gly	Ser	Ile	Asn	Glu	Ser	Pro	Ile	Glu	Glu	His	Met	Asn	Asp
1				5					10				15		
Ser	Pro	Ser	Thr	Lys	Glu	Lys	Ala	Asp	Ser	Val	Asp	Ile	Ser	Asp	Tyr
				20					25				30		
Ile	Val	Ser	His	Ser	Asp	Asp	Ser	Leu	Ser	Lys	Asp	Ile	Lys	Lys	Asp
				35				40				45			
Thr	Lys	Ser	Phe	Leu	Asp	Val	Glu	His	Gly	Glu	Ile	Ser	Thr	Val	Asp
	50				55					60					
Glu	Phe	Glu	Glu	Asp	Ser	Pro	Tyr	Pro	Glu	Val	Arg	Ala	Ala	Val	Pro
65					70				75				80		
Pro	Thr	Asp	Asp	Pro	Ser	Met	Pro	Cys	Asn	Thr	Ile	Arg	Met	Trp	Thr
						85			90				95		
Ile	Gly	Leu	Ile	Tyr	Ser	Thr	Val	Gly	Ala	Ala	Val	Asn	Met	Phe	Phe
				100				105					110		
Ser	Leu	Arg	Asn	Pro	Thr	Val	Thr	Leu	Ser	Val	Leu	Ile	Ser	Glu	Leu
				115				120				125			
Leu	Ala	Tyr	Pro	Ala	Leu	Gln	Ile	Trp	Asp	Leu	Ile	Phe	Pro	Asp	Arg
130					135					140					
Glu	Phe	Arg	Ile	Gly	Arg	Leu	Lys	Phe	Asn	Phe	Lys	Pro	Gly	Pro	Phe
145					150				155				160		
Asn	Val	Lys	Glu	His	Ala	Leu	Ile	Val	Val	Met	Ser	Ser	Val	Ser	Phe
					165				170				175		
Gly	Asn	Ala	Tyr	Ser	Thr	Asp	Ile	Ile	Leu	Ala	Gln	Arg	Val	His	Tyr
				180				185				190			
Lys	Gln	Arg	Phe	Gly	Phe	Gly	Tyr	Glu	Ile	Cys	Leu	Thr	Leu	Ala	Thr
					195			200				205			
Gln	Leu	Ile	Gly	Tyr	Gly	Leu	Ala	Gly	Leu	Ser	Arg	Arg	Leu	Leu	Val
						210			215				220		
Arg	Pro	Ala	Ser	Met	Leu	Trp	Pro	Val	Asn	Leu	Val	Gln	Cys	Thr	Leu
225					230				235				240		
Ile	Lys	Thr	Leu	His	Arg	Lys	Asp	Leu	Arg	Asn	Ala	Val	Ala	Asn	Gly
					245				250				255		
Trp	Arg	Ile	Ser	Pro	Phe	Arg	Phe	Phe	Leu	Tyr	Val	Phe	Ile	Ala	Ser
				260				265				270			
Phe	Ile	Trp	Asn	Trp	Phe	Pro	Ser	Tyr	Ile	Phe	Gln	Ala	Leu	Ser	Leu
					275			280				285			

Phe Ala Trp Val Thr Trp Ile Arg Pro Asn Ser Pro Thr Val Asn Gln
290 295 300

Ile Phe Gly Glu Ser Thr Gly Ile Ser Ile Leu Pro Met Thr Phe Asp
305 310 315 320

Trp Asn Gln Ile Ser Ala Tyr Ile Leu Ser Pro Leu Met Ala Pro Ala
325 330 335

Asp Ala Leu Met Asn Ile Leu Leu Gly Val Ile Leu Phe Phe Trp Ile
340 345 350

Val Thr Pro Ala Leu Asn Phe Thr Asn Thr Trp Tyr Gly Asp Tyr Leu
355 360 365

Pro Ile Ser Ser Ser Gly Ile Ile Asp His Phe Gly Asn Ser Tyr Asn
370 375 380

Val Thr Arg Ile Leu Thr Lys Asp Ala Thr Phe Asp Leu Asp Ala Tyr
385 390 395 400

Gln Asn Tyr Ser Pro Ile Phe Met Ser Thr Thr Tyr Ala Leu Ala Phe
405 410 415

Gly Leu Ser Phe Ala Ser Ile Thr Ser Val Ile Phe His Val Ile Leu
420 425 430

Tyr His Gly Lys Glu Ile Tyr Asp Arg Leu Arg Asp Pro Pro Ala Pro
435 440 445

Asp Ile His Glu Lys Leu Met Lys Ala Tyr Asp Glu Val Pro Phe Tyr
450 455 460

Trp Tyr Leu Ser Val Phe Leu Ala Phe Phe Gly Met Met Met Gly Thr
465 470 475 480

Ile Tyr Gly Trp Lys Thr Glu Thr Pro Trp Trp Val Ile Ile Val Gly
485 490 495

Val Ile Phe Ser Ala Val Trp Phe Ile Pro Ile Gly Ile Val Gln Ala
500 505 510

Ile Thr Asn Ile Gln Leu Gly Leu Asn Val Phe Thr Glu Phe Ile Val
515 520 525

Gly Tyr Met Tyr Pro Gly Arg Pro Leu Ala Met Met Ile Phe Lys Thr
530 535 540

Val Gly Tyr Ile Thr Met Thr Gln Gly Leu Ala Phe Ala Ala Asp Leu
545 550 555 560

Lys Phe Gly His Tyr Met Lys Leu Pro Pro Arg Ile Met Phe Tyr Thr
565 570 575

Gln Met Ile Ala Thr Ile Trp Ser Cys Phe Val Gln Ile Gly Val Leu
580 585 590

Asp Trp Ala Leu Gly Asn Ile Asp Asn Val Cys Gln Ala Asp Gln Pro
595 600 605

Asp Asn Tyr Thr Cys Pro Asn Ala Thr Val Phe Phe Asn Ser Ser Val
610 615 620

Ile Trp Gly Val Ile Gly Pro Lys Arg Met Phe Ser Gly Lys Asn Thr
625 630 635 640

Tyr Thr Gly Leu Gln Tyr Phe Trp Leu Ala Gly Val Leu Gly Thr Ile
645 650 655

Leu Phe Trp Ala Leu Trp Lys Lys Trp Pro Gln Lys Trp Trp Gly Gln
660 665 670

Leu Asn Gly Pro Leu Ile Phe Gly Gly Thr Gly Tyr Ile Pro Pro Ala
675 680 685

Thr Pro Val Asn Tyr Leu Ala Trp Ser Gly Ile Gly Leu Phe Phe Asn
690 695 700

Tyr Tyr Leu Lys Lys Ile Phe Ala Asp Trp Trp Gln Lys Tyr Asn Phe
705 710 715 720

Thr Leu Ser Ala Leu Asp Thr Gly Thr Gln Leu Ser Val Ile Ile Leu
725 730 735

Phe Phe Cys Leu Gln Leu Pro Met Val Asn Phe Pro Asp Trp Trp Gly
740 745 750

Asn Asp Gly Ala Phe Asn Thr Leu Asp Ala Thr Gly Ala Ala Val Arg
755 760 765

Lys Leu Val Asn Glu Ser Ala Arg
770 775

<210> 14
<211> 783
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: Opt1

<400> 14
Met Asp Lys Ile Arg Ala Val Ile Ser Gly Gly Glu Lys Pro Pro Val
1 5 10 15

Asp Thr Asp Asn Asp His Asn Thr Asp Phe Glu Ala Asp Arg Lys Met
20 25 30

Pro Asp Leu Asp Ile Val Val Ser Lys Ser Gln Glu Phe Asp Pro Val
35 40 45

Thr Ser His Leu Val Asn Asp Ile Met Glu Asp Glu Tyr Ala Ala Val
50 55 60

His Val Glu Asp Asp Ser Pro Tyr Pro Glu Val Arg Ala Ala Val Pro
65 70 75 80

Ser Thr Asp Asp Pro Thr Leu Pro Gln Asn Thr Ile Arg Ala Trp Val
85 90 95

Ile Gly Leu Ile Leu Thr Thr Val Gly Cys Gly Met Asn Met Leu Phe
100 105 110

Ser Phe His Ser Pro Ser Phe Ala Ile Thr Thr Phe Val Thr Ser Ile
115 120 125

Leu Ala Trp Pro Ile Gly Asn Phe Trp Ala Trp Ile Val Pro Asp Trp
130 135 140

Lys Ile Phe Gly Ala Ser Leu Asn Pro Gly Pro Phe Asn Val Lys Glu
145 150 155 160

His Thr Ile Ile Thr Ile Met Ala Asn Val Ser Phe Gly Thr Gly Ala
165 170 175

Ala Tyr Ala Thr Asp Ile Leu Leu Ala Gln Asn Met Phe Tyr Lys Ser
180 185 190

Asn Phe Gly Trp Gly Tyr Asn Leu Leu Leu Ile Trp Ser Thr Gln Cys
195 200 205

Ile Gly Phe Ala Phe Gly Gly Val Met Arg Arg Phe Val Val Asp Ser
210 215 220

Pro Gly Ala Ile Trp Pro Leu Asn Leu Val Thr Ala Thr Phe Leu Thr
225 230 235 240

Asn Met His Ile Asn Glu Asn His Thr Ala Asn Gly Trp Lys Ile Ser
245 250 255

Arg Leu Ala Phe Phe Val Ile Val Phe Val Ala Ser Phe Val Trp Tyr
260 265 270

Trp Phe Pro Gly Tyr Ile Phe Gln Ala Leu Ser Tyr Phe Ser Trp Ile
275 280 285

Thr Trp Ile Lys Pro Asn Asn Val Ile Ile Asn Gln Val Phe Gly Ser
290 295 300

Ser Ser Gly Leu Gly Met Ile Pro Asn Asn Ile Ala Leu Asp Trp Asn
305 310 315 320

Gln Ile Ala Gly Tyr Ile Gly Ser Pro Leu Ile Pro Pro Ala Ser Val
325 330 335

Ile Ala Thr Ile Phe Gly Ser Ile Val Leu Ile Phe Trp Ile Val Val
340 345 350

Pro Ala Ile His Tyr Ser Asn Thr Trp Tyr Ser Gln Tyr Leu Pro Ile
355 360 365

Ser Ser Thr Gly Ser Phe Asp Arg Phe Gln Gln Thr Tyr Asn Val Ser
370 375 380

Lys Ile Ile Asp His Lys Thr Leu Ser Phe Asn Glu Ala Glu Tyr Lys
385 390 395 400

Lys Tyr Ser Pro Leu Phe Leu Ser Thr Thr Phe Ala Ile Ser Tyr Gly
405 410 415

Leu Ser Phe Ala Ser Ile Leu Ala Thr Ile Thr His Thr Ile Cys Phe

420 425 430

His Gly Arg Asp Leu Ile Ala Ser Leu Lys Ala Lys Glu Lys Pro Asp
435 440 445

Val His Asn Arg Leu Met Lys Ala Tyr Lys Pro Val Pro Glu Trp Trp
450 455 460

Tyr Leu Val Val Phe Leu Val Phe Phe Gly Met Ser Ile Ala Thr Val
465 470 475 480

Arg Ala Trp Pro Thr Glu Met Pro Val Trp Gly Leu Val Phe Ala Leu
485 490 495

Ile Ile Ala Ile Ile Phe Leu Leu Pro Val Ala Ile Ile Tyr Ala Lys
500 505 510

Thr Asn Ile Ala Val Gly Leu Asn Val Val Thr Glu Phe Ile Val Gly
515 520 525

Tyr Val Leu Gly Gly Arg Pro Leu Cys Met Met Leu Phe Lys Thr Phe
530 535 540

Gly Tyr Ile Thr Asn Asn Gln Ala Val Thr Phe Val Gln Asp Met Lys
545 550 555 560

Leu Gly His Tyr Met Lys Ile Asp Pro Arg Thr Leu Phe Trp Ala Gln
565 570 575

Phe Ala Ala Thr Ile Trp Gly Ser Leu Val Gln Ile Ala Val Leu Glu
580 585 590

Trp Ala Val Gly Ala Ile Asp Asn Leu Cys Ala Ala Asp Gln Lys Asn
595 600 605

His Tyr Thr Cys Pro Asn Gly Lys Val Phe Phe Asn Ala Ser Ile Ile
610 615 620

Trp Gly Val Ile Gly Pro Gln Arg Gln Phe Ser His Gly Gln Ile Tyr
625 630 635 640

Tyr Gly Leu Leu Phe Phe Ile Ile Gly Ala Val Thr Pro Val Ile
645 650 655

Asn Trp Leu Ile Leu Lys Lys Trp Pro Asn Ser Pro Val Lys Tyr Leu
660 665 670

His Trp Pro Val Phe Phe Ser Gly Thr Gly Tyr Ile Pro Pro Ala Thr
675 680 685

Pro Tyr Asn Tyr Thr Ser Tyr Cys Ala Val Gly Leu Phe Phe Gly Trp
690 695 700

Trp Ile Lys Lys Lys Trp Phe His Trp Trp Ser Lys Tyr Asn Tyr Ser
705 710 715 720

Leu Ser Ala Gly Leu Asp Ile Gly Leu Ala Trp Cys Ser Leu Ile Ile
725 730 735

Phe Leu Cys Leu Ser Leu Thr Asn Thr Asp Phe Pro Ser Trp Trp Gly
740 745 750

Asn Asp Val Ile Asn Thr Thr Leu Asp Thr Gln Val Val Thr Asn Ile
755 760 765

Arg His Ile Leu Lys Glu Gly Glu Ala Phe Gly Pro Ser Ser Trp
770 775 780

<210> 15

<211> 798

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: YJL212C

<400> 15

Met Ser Thr Ile Tyr Arg Glu Ser Asp Ser Leu Glu Ser Glu Pro Ser
1 5 10 15

Pro Thr Pro Thr Ile Pro Ile Gln Ile Asn Met Glu Glu Glu Lys
20 25 30

Lys Asp Ala Phe Val Lys Asn Ile Asp Glu Asp Val Asn Asn Leu Thr
35 40 45

Ala Thr Thr Asp Glu Glu Asp Arg Asp Pro Glu Ser Gln Lys Phe Asp
50 55 60

Arg His Ser Ile Gly Glu Glu Gly Leu Val Trp Lys Gly Asp Pro Thr
65 70 75 80

Tyr Leu Pro Asn Ser Pro Tyr Pro Glu Val Arg Ser Ala Val Ser Ile
85 90 95

Glu Asp Asp Pro Thr Ile Arg Leu Asn His Trp Arg Thr Trp Phe Leu
100 105 110

Thr Thr Val Phe Val Val Val Phe Ala Gly Val Asn Gln Phe Phe Ser
115 120 125

Leu Arg Tyr Pro Ser Leu Glu Ile Asn Phe Leu Val Ala Gln Val Val
130 135 140

Cys Tyr Pro Ile Gly Arg Ile Ala Leu Leu Pro Asp Trp Lys Cys Ser
145 150 155 160

Lys Val Pro Phe Phe Asp Leu Asn Pro Gly Pro Phe Thr Lys Lys Glu
165 170 175

His Ala Val Val Thr Ile Ala Val Ala Leu Thr Ser Ser Thr Ala Tyr
180 185 190

Ala Met Tyr Ile Leu Asn Ala Gln Gly Ser Phe Tyr Asn Met Lys Leu
195 200 205

Asn Val Gly Tyr Gln Phe Leu Leu Val Trp Thr Ser Gln Met Ile Gly
210 215 220

Tyr Gly Ala Ala Gly Leu Thr Arg Arg Trp Val Val Asn Pro Ala Ser
225 230 235 240

Ser Ile Trp Pro Gln Thr Leu Ile Ser Val Ser Leu Phe Asp Ser Leu
245 250 255

His Ser Arg Lys Val Glu Lys Thr Val Ala Asn Gly Trp Thr Met Pro
260 265 270

Arg Tyr Arg Phe Phe Leu Ile Val Leu Ile Gly Ser Phe Ile Trp Tyr
275 280 285

Trp Val Pro Gly Phe Leu Phe Thr Gly Leu Ser Tyr Phe Asn Val Ile
290 295 300

Leu Trp Gly Ser Lys Thr Arg His Asn Phe Ile Ala Asn Thr Ile Phe
305 310 315 320

Gly Thr Gln Ser Gly Leu Gly Ala Leu Pro Ile Thr Phe Asp Tyr Thr
325 330 335

Gln Val Ser Gln Ala Met Ser Gly Ser Val Phe Ala Thr Pro Phe Tyr
340 345 350

Val Ser Ala Asn Thr Tyr Ala Ser Val Leu Ile Phe Phe Val Ile Val
355 360 365

Leu Pro Cys Leu Tyr Phe Thr Asn Thr Trp Tyr Ala Lys Tyr Met Pro
370 375 380

Val Ile Ser Gly Ser Thr Tyr Asp Asn Thr Gln Asn Lys Tyr Asn Val
385 390 395 400

Thr Lys Ile Leu Asn Glu Asp Tyr Ser Ile Asn Leu Glu Lys Tyr Lys
405 410 415

Glu Tyr Ser Pro Val Phe Val Pro Phe Ser Tyr Leu Leu Ser Tyr Ala
420 425 430

Leu Asn Phe Ala Ala Val Ile Ala Val Phe Val His Cys Ile Leu Tyr
435 440 445

His Gly Lys Asp Ile Val Ala Lys Phe Lys Asp Arg Lys Asn Gly Gly
450 455 460

Thr Asp Ile His Met Arg Ile Tyr Ser Lys Asn Tyr Lys Asp Cys Pro
465 470 475 480

Asp Trp Trp Tyr Leu Leu Leu Gln Ile Val Met Ile Gly Leu Gly Phe
485 490 495

Val Ala Val Cys Cys Phe Asp Thr Lys Phe Pro Ala Trp Ala Phe Val
500 505 510

Ile Ala Ile Leu Ile Ser Leu Val Asn Phe Ile Pro Gln Gly Ile Leu
515 520 525

Glu Ala Met Thr Asn Gln His Val Gly Leu Asn Ile Ile Thr Glu Leu
530 535 540

Ile Cys Gly Tyr Met Leu Pro Leu Arg Pro Met Ala Asn Leu Leu Phe
545 550 555 560

Lys Leu Tyr Gly Phe Ile Val Met Arg Gln Gly Leu Asn Leu Ser Arg
565 570 575

Asp Leu Lys Leu Ala Met Tyr Met Lys Val Ser Pro Arg Leu Ile Phe
580 585 590

Ala Val Gln Ile Tyr Ala Thr Ile Ile Ser Gly Met Val Asn Val Gly
595 600 605

Val Gln Glu Trp Met Met His Asn Ile Asp Gly Leu Cys Thr Thr Asp
610 615 620

Gln Pro Asn Gly Phe Thr Cys Ala Asn Gly Arg Thr Val Phe Asn Ala
625 630 635 640

Ser Ile Ile Trp Ser Leu Pro Lys Tyr Leu Phe Ser Ser Gly Arg Ile
645 650 655

Tyr Asn Pro Leu Met Trp Phe Phe Leu Ile Gly Leu Leu Phe Pro Leu
660 665 670

Ala Val Tyr Ala Val Gln Trp Lys Phe Pro Lys Phe Lys Phe Ala Lys
675 680 685

His Ile His Thr Pro Val Phe Phe Thr Gly Pro Gly Asn Ile Pro Pro
690 695 700

Ser Thr Pro Tyr Asn Tyr Ser Leu Phe Phe Ala Met Ser Phe Cys Leu
705 710 715 720

Asn Leu Ile Arg Lys Arg Trp Arg Ala Trp Phe Asn Lys Tyr Asn Phe
725 730 735

Val Met Gly Ala Gly Val Glu Ala Gly Val Ala Ile Ser Val Val Ile
740 745 750

Ile Phe Leu Cys Val Gln Tyr Pro Gly Gly Lys Leu Ser Trp Trp Gly
755 760 765

Asn Asn Val Trp Lys Arg Thr Tyr Asp Asn Asp Tyr Lys Lys Phe Tyr
770 775 780 785

Thr Leu Lys Lys Gly Glu Thr Phe Gly Tyr Asp Lys Trp Trp
790 795

<210> 16
<211> 877
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: YPR194C

<400> 16
Met Ser Glu Thr Tyr Lys Asp Lys Val Ile Ile Asp Glu Lys Val Ser
1 5 10 15

Thr Lys Gly Thr Val Asp Tyr Ala Glu Gly Ala Glu Tyr Ser Glu Arg
20 25 30

Leu Ser Asn His Ser Ser Asp Phe Ser Gln Trp Tyr Thr Asp Glu Gln
35 40 45

Ile Leu His Phe Met Lys Lys Leu Gly Tyr Glu Asn Arg Thr Leu Val
50 55 60

Asp Ile Pro Glu Asp Val Ala Tyr Ile Leu Lys Lys Met Pro Glu Leu
65 70 75 80

Thr Leu Glu Asp Ser Phe Lys Ile Leu Lys Asp Ser Ile Ile Tyr Phe
85 90 95

Lys Asp Asp Glu Asn Ile Pro His Asp Gln Tyr Glu Glu Trp Lys Arg
100 105 110

Leu Val Asp Leu Glu Asp Leu Asp Ser Lys Glu Gly Ile Asp Glu Tyr
115 120 125

Asp Ser Phe Asp Ile Arg Ala Phe Ala Ser Ala Ile Lys Phe His Ser
130 135 140

Pro Tyr Gln Glu Val Arg Ala Val Val Asp Pro Glu Asp Asp Pro Thr
145 150 155 160

Ile Pro Val Glu Thr Phe Arg Ala Tyr Phe Leu Ala Ile Ile Trp Ser
165 170 175

Val Ile Gly Ser Gly Phe Asn Glu Phe Phe Ser His Arg Val Val Ser
180 185 190

Ile Ser Leu Asn Thr Pro Ile Ile Gln Met Phe Leu Tyr Ile Cys Gly
195 200 205

Lys Ala Trp Ala Lys Thr Ile Pro Cys Trp Thr Ile Thr Ile Arg Gly
210 215 220

Arg Lys Tyr Gly Ile Asn Ile Asp Lys Pro Trp Thr Gln Lys Glu Gln
225 230 235 240

Met Phe Ser Thr Leu Leu Tyr Ala Ile Cys Gln Gly Ala Phe Tyr Thr
245 250 255

His Tyr Asn Ile Leu Thr Gln Lys Leu Phe Tyr His Ser Ala Phe Ser
260 265 270

Phe Gly Tyr Gln Phe Leu Leu Ser Leu Ser Val Gln Phe Ile Gly Phe
275 280 285

Gly Phe Ala Gly Ile Leu Arg Lys Phe Val Val Tyr Pro Ala Arg Ala
290 295 300

Leu Trp Pro Thr Val Met Pro Thr Ile Ala Ile Asn Lys Ala Leu Leu
305 310 315 320

Gly Lys Glu Lys His Glu Ser Gly Met Ser Arg Tyr Lys Phe Phe Phe
325 330 335

Leu Thr Phe Phe Ile Met Phe Ile Tyr Asn Trp Phe Pro Thr Tyr Ile
340 345 350

Ile Asn Ile Leu Asn Thr Phe Asn Trp Met Thr Trp Ile Lys Pro Ser

355 360 365
Asn Ile Asn Leu Ala Asn Ile Thr Gly Gly Val Thr Gly Leu Gly Ile
370 375 380
Asn Pro Ile Ser Ser Phe Asp Trp Asn Val Ile Ser Phe Asn Ser Pro
385 390 400
Leu Val Tyr Pro Phe Trp Ser Tyr Leu Thr Gln Tyr Leu Gly Cys Ile
405 410 415
Leu Ala Ala Leu Ile Val Ile Ala Val Tyr Tyr Ser Asn Tyr Met Ser
420 425 430
Cys Gln Tyr Leu Pro Ile Phe Thr Asn Ser Leu Tyr Thr Asn Thr Gly
435 440 445
His Ser Phe Lys Val Thr Glu Val Leu Asp Ser Asp Asn Lys Leu Asp
450 455 460
Val Lys Lys Tyr Gln Ser Tyr Ser Pro Pro Tyr Tyr Ser Ala Gly Asn
465 470 475 480
Leu Val Ser Tyr Gly Ala Phe Ile Cys Ala Tyr Pro Leu Met Ile Thr
485 490 495
Trp Ser Phe Ile Val His Ser Lys Leu Leu Phe Asn Ala Phe Lys Asp
500 505 510
Trp Ala Leu Asn Leu Trp Ala Met Arg Lys Leu Lys Ser Trp Val Thr
515 520 525
Met Phe Lys Ser Asp Tyr Arg Ala Leu Asp Asp Tyr Asp Asp Pro His
530 535 540
Ser Asn Ala Met Lys Asn Tyr Lys Glu Val Pro Asp Trp Trp Tyr Phe
545 550 555 560
Ala Ile Leu Ile Gly Ser Leu Val Val Gly Ile Ala Val Val Glu His
565 570 575
Tyr Pro Thr Asn Thr Pro Val Trp Gly Leu Phe Val Cys Leu Gly Phe
580 585 590
Asn Phe Val Phe Leu Ile Pro Thr Thr Ile Leu Gln Ala Thr Thr Gly
595 600 605
Tyr Ser Phe Gly Leu Asn Leu Ile Glu Met Val Met Gly Tyr Ala
610 615 620
Leu Pro Gly Asn Pro Ile Ala Ile Met Ile Leu Lys Ala Phe Gly Tyr
625 630 635 640
Asn Ile Asp Gly Gln Ala Asp Asn Tyr Val Ser Asn Leu Lys Ile Ala
645 650 655
His Tyr Cys Lys Ile Pro Pro Met Ala Leu Phe Arg Gly Gln Cys Val
660 665 670
Ile Val Phe Ile Gln Ile Phe Val Asn Leu Gly Val Leu Asn Trp Gln
675 680 685

Ile Ser Asn Ile Lys Asp Phe Cys Thr Pro His Gln Asn Ala Lys Phe
690 695 700

Thr Cys Pro Asp Ala Val Thr Tyr Tyr Asn Ala Ser Val Val Trp Gly
705 710 715 720

Ala Ile Gly Pro Lys Arg Ile Phe Asn Tyr Ile Tyr Pro Ile Phe Lys
725 730 735

Trp Cys Trp Leu Ile Gly Ala Cys Ile Gly Ile Phe Phe Gly Val Trp
740 745 750

Lys Arg Trp Gly Lys Phe Tyr Pro Arg Tyr Phe Asp Pro Met Leu Phe
755 760 765

Val Gly Gly Met Leu Asn Met Ser Pro Pro Tyr Asn Leu Met Tyr Tyr
770 775 780

Thr Ser Gly Met Ile Val Ser Tyr Ile Ser Gln Tyr Tyr Met Lys Arg
785 790 795 800

His His Leu Asn Leu Trp Glu Lys Tyr Asn Tyr Val Leu Ser Ala Gly
805 810 815

Phe Ser Thr Gly Leu Val Leu Ser Ala Ile Ile Ile Phe Phe Ala Val
820 825 830

Gln Tyr Lys Asp Thr Ala Phe Asn Trp Trp Gly Asn Thr Val Pro Tyr
835 840 845

Ala Gly Ala Asp Gly Val Gly Tyr Pro Leu Lys Asn Ile Thr Asp Thr
850 855 860

Ala Asn Gly Tyr Phe Gly Tyr Ala Pro Gly His Tyr Pro
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<211> 2634
<212> DNA
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: OPT

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<210> 18

<211> 5

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Leu Enkphalin

<400> 18

Tyr Gly Gly Phe Met

1 5

<210> 19

<211> 5

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Met Enkephalin

<400> 19

Tyr Gly Gly Phe Leu

1 5

<210> 20

<211> 4

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: uptake peptide

<400> 20
Gly Gly Phe Leu
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<210> 21
<211> 4
<212> PRT
<213> Unknown Organism

<220>

<223> Description of Unknown Organism: uptake peptide

<400> 21
Lys Leu Gly Leu
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<210> 22
<211> 4
<212> PRT
<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Tyr-Mif-1

<400> 22
Tyr Pro Leu Gly
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<210> 23
<211> 5
<212> PRT
<213> Unknown Organism

<220>

<223> Description of Unknown Organism: uptake peptide

<400> 23
Tyr Gly Gly Phe Leu
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<210> 24
<211> 7
<212> PRT
<213> Unknown Organism

<220>

<223> Description of Unknown Organism: DPDPE

<220>

<221> MOD_RES
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<223> Pen

<220>
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<400> 24
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<210> 25
<211> 7
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: DADLE

<400> 25
Tyr Asp Ala Gly Phe Asp Leu
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<210> 26
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: motif

<220>
<223> Xaa represents a variable amino acid

<400> 26
Ser Pro Tyr Xaa Glu Val Arg Xaa Xaa Val Xaa Xaa Xaa Asp Asp Pro
1 5 10 15